CLEAN COPY OF CLAIMS FOR SERIAL NO. 09/533,466

WE CLAIM:

1. A crystal of IMPDH (ionisine monophosphate dehydrogenase) isolated from a bacterial preparation.

2. The crystal of claim 1 further characterized by ability to provide x-ray diffraction patterns useful to define molecular structures for bacterial IMPDH enzymes.

3. A crystal of IMPDH (ionisine monophosphate dehydrogenase) isolated from a bacterial preparation wherein the bacterial preparation is a pure culture of *Streptococcus pyogenes*.

4. A method for designing inhibitors of bacterial IMPDH (inosine monophosphate dehydrogenase), said method comprising:

   a. obtaining a crystal of bacterial IMPDH;

   b. recording x-ray diffraction data from said crystal;

   c. using said diffraction data to generate an electron density map consistent with a model for the molecular structure of a binding pocket of IMPDH; and

   d. designing inhibitors of bacterial IMPDH based on the map of three dimensional structural information of the molecular structure of the binding pocket of IMPDH.

5. A crystalline molecule or molecular complex comprising an IMPDH binding pocket defined by the structural coordinates of IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-433, and 449-455 according to Table 7 or a homologue of said molecule or molecular complex.

6. A crystalline molecule or molecular complex comprising all or any parts of a binding pocket defined by structure coordinates of IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-432 and 449-455, according to Table 7, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has an amino acid sequence identity for the corresponding binding pocket residues of 60% or greater relative to the *S. pyogenes* IMPDH binding pocket.

7. A crystalline IMPDH molecule defined by structural coordinates for IMPDH amino acids from *S. pyogenes* IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-433, and 449-455.

8. A crystalline IMPDH molecule having (inosine monophosphate) IMP in its binding pocket.

15. A computer generated representation of a molecule or molecular complex comprising a binding pocket defined by the following structural coordinates of *S. pyogenes* IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-433, and 449-455.